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P#12

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## RAW SEQUENCE LISTING

DATE: 06/18/2003

PATENT APPLICATION: US/10/056,052A

TIME: 11:44:16

Input Set : A:\Sequence\_10-056,152.txt

Output Set: N:\CRF4\06182003\J056052A.raw

C--> 2 <110> APPLICANT: PATTI, Joseph M  
3 HUTCHINS, Jeff T  
4 DOMANSKI, Paul  
5 PATEL, Pratiksha  
6 HALL, Andrea  
8 <120> TITLE OF INVENTION: MONOCLONAL ANTIBODIES TO THE CLFA PROTEIN . . .  
10 <130> FILE REFERENCE: P07069US04/BAS  
12 <140> CURRENT APPLICATION NUMBER: 10/056,052A  
13 <141> CURRENT FILING DATE: 2002-01-18  
15 <150> PRIOR APPLICATION NUMBER: 60/308,116  
16 <151> PRIOR FILING DATE: 2001-07-30  
18 <150> PRIOR APPLICATION NUMBER: 60/298,413  
19 <151> PRIOR FILING DATE: 2001-06-18  
21 <150> PRIOR APPLICATION NUMBER: 60/274,611  
22 <151> PRIOR FILING DATE: 2001-03-12  
24 <150> PRIOR APPLICATION NUMBER: 60/264,072  
25 <151> PRIOR FILING DATE: 2001-01-26  
27 <160> NUMBER OF SEQ ID NOS: 29  
29 <170> SOFTWARE: PatentIn version 3.1  
31 <210> SEQ ID NO: 1  
32 <211> LENGTH: 1560  
33 <212> TYPE: DNA  
34 <213> ORGANISM: Staphylococcus aureus  
36 <400> SEQUENCE: 1  
37 agtgaataa gtgttacgca atctgatagc gcaagtaacg aaagcaaaag taatgattca 60  
39 agtagcgta gtgctgcacc taaaacagac gacacaaacg tgagtgtacg taaaacatcg 120  
41 tcaaacacta ataattggcg aacgagtggt ggcgcaaatc cagcacaaca ggaaacgaca 180  
43 caatcatcat caacaaatgc aactacggaa gaaacgcggg taactggtga agctactact 240  
45 acgacaacga atcaagctaa tacaccggca acaactcaat caagcaatac aaatgcggag 300  
47 gaattagtga atcaaacaaag taatgaaacg acttttaatg atactaatac agtatcatct 360  
49 gtaaatccac ctcaaaattc tacaatgctg gaaaatgttt caacaacgca agataacttca 420  
51 actgaagcaa caccttcaaa caatgaatca gctccacaga gtacagatgc aagtaataaa 480  
53 gatgtagtta atcaagcggg taatacaagt ggcgcctaga tgagagcatt tagtttagcg 540  
55 gcagtagctg cagatgcacc ggcagctggc acagatatta cgaatcagtt gacgaatgtg 600  
57 acagtttgga ttgactctgg tacgactgtg tatccgcacc aagcaggtta tgtcaaaactg 660  
59 aattatgggt ttctagtgcc taattctgct gttaaagggt acacattcaa aataactgta 720  
61 cctaaagaat taaacttaaa tgggtgaact tcaactgcta aagtgccacc aattatggct 780  
63 ggagatcaag tattggcaaa tgggtgaatc gatagtgatg gtaatgttat ttatacattt 840  
65 acagactatg taaatactaa agatgatgta aaagcaactt tgaccatgcc cgcttatatt 900  
67 gaccctgaaa atgttaaaaa gacaggtaat gtgacattgg ctactggcat aggtagtaca 960  
69 acagcaaaaca aaacagtatt agtagattat gaaaaatatg gtaagtttta taacttatct 1020  
71 attaaaggta caattgacca aatcgataaa acaaataata cgtatcgtca gacaatttat 1080  
73 gtcaatccaa gtggagataa cgttattgct ccggttttaa caggtaattt aaaaccaa 1140

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75 acggatagta atgcattaat agatcagcaa aatacaagta ttaaagtata taaagtagat 1200
77 aatgcagctg atttatctga aagttacttt gtgaatccag aaaactttga ggatgtcact 1260
79 aatagtgtga atattacatt cccaaatcca aatcaatata aagtagagtt taatacgctt 1320
81 gatgatcaaa ttacaacacc gtatatagta gttgttaatg gtcataattga tccgaatagc 1380
83 aaaggtgatt tagctttacg ttcaacttta tatgggtata actcgaatat aatttggcgc 1440
85 tctatgtcat gggacaacga agtagcattt aataacggat caggttctgg tgacgggtatc 1500
87 gataaaccag ttgttcctga acaacctgat gagcctggtg aaattgaacc aattccagag 1560
90 <210> SEQ ID NO: 2
91 <211> LENGTH: 520
92 <212> TYPE: PRT
93 <213> ORGANISM: Staphylococcus aureus
95 <400> SEQUENCE: 2
97 Ser Glu Asn Ser Val Thr Gln Ser Asp Ser Ala Ser Asn Glu Ser Lys
98 1 5 10 15
101 Ser Asn Asp Ser Ser Ser Val Ser Ala Ala Pro Lys Thr Asp Asp Thr
102 20 25 30
105 Asn Val Ser Asp Thr Lys Thr Ser Ser Asn Thr Asn Asn Gly Glu Thr
106 35 40 45
109 Ser Val Ala Gln Asn Pro Ala Gln Gln Glu Thr Thr Gln Ser Ser Ser
110 50 55 60
113 Thr Asn Ala Thr Thr Glu Glu Thr Pro Val Thr Gly Glu Ala Thr Thr
114 65 70 75 80
117 Thr Thr Thr Asn Gln Ala Asn Thr Pro Ala Thr Thr Gln Ser Ser Asn
118 85 90 95
121 Thr Asn Ala Glu Glu Leu Val Asn Gln Thr Ser Asn Glu Thr Thr Phe
122 100 105 110
125 Asn Asp Thr Asn Thr Val Ser Ser Val Asn Ser Pro Gln Asn Ser Thr
126 115 120 125
129 Asn Ala Glu Asn Val Ser Thr Thr Gln Asp Thr Ser Thr Glu Ala Thr
130 130 135 140
133 Pro Ser Asn Asn Glu Ser Ala Pro Gln Ser Thr Asp Ala Ser Asn Lys
134 145 150 155 160
137 Asp Val Val Asn Gln Ala Val Asn Thr Ser Ala Pro Arg Met Arg Ala
138 165 170 175
141 Phe Ser Leu Ala Ala Val Ala Ala Asp Ala Pro Ala Ala Gly Thr Asp
142 180 185 190
145 Ile Thr Asn Gln Leu Thr Asn Val Thr Val Gly Ile Asp Ser Gly Thr
146 195 200 205
149 Thr Val Tyr Pro His Gln Ala Gly Tyr Val Lys Leu Asn Tyr Gly Phe
150 210 215 220
153 Ser Val Pro Asn Ser Ala Val Lys Gly Asp Thr Phe Lys Ile Thr Val
154 225 230 235 240
157 Pro Lys Glu Leu Asn Leu Asn Gly Val Thr Ser Thr Ala Lys Val Pro
158 245 250 255
161 Pro Ile Met Ala Gly Asp Gln Val Leu Ala Asn Gly Val Ile Asp Ser
162 260 265 270
165 Asp Gly Asn Val Ile Tyr Thr Phe Thr Asp Tyr Val Asn Thr Lys Asp
166 275 280 285
169 Asp Val Lys Ala Thr Leu Thr Met Pro Ala Tyr Ile Asp Pro Glu Asn

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170      290      295      300
173 Val Lys Lys Thr Gly Asn Val Thr Leu Ala Thr Gly Ile Gly Ser Thr
174 305      310      315      320
177 Thr Ala Asn Lys Thr Val Leu Val Asp Tyr Glu Lys Tyr Gly Lys Phe
178      325      330      335
181 Tyr Asn Leu Ser Ile Lys Gly Thr Ile Asp Gln Ile Asp Lys Thr Asn
182      340      345      350
185 Asn Thr Tyr Arg Gln Thr Ile Tyr Val Asn Pro Ser Gly Asp Asn Val
186      355      360      365
189 Ile Ala Pro Val Leu Thr Gly Asn Leu Lys Pro Asn Thr Asp Ser Asn
190      370      375      380
193 Ala Leu Ile Asp Gln Gln Asn Thr Ser Ile Lys Val Tyr Lys Val Asp
194 385      390      395      400
197 Asn Ala Ala Asp Leu Ser Glu Ser Tyr Phe Val Asn Pro Glu Asn Phe
198      405      410      415
201 Glu Asp Val Thr Asn Ser Val Asn Ile Thr Phe Pro Asn Pro Asn Gln
202      420      425      430
205 Tyr Lys Val Glu Phe Asn Thr Pro Asp Asp Gln Ile Thr Thr Pro Tyr
206      435      440      445
209 Ile Val Val Val Asn Gly His Ile Asp Pro Asn Ser Lys Gly Asp Leu
210      450      455      460
213 Ala Leu Arg Ser Thr Leu Tyr Gly Tyr Asn Ser Asn Ile Ile Trp Arg
214 465      470      475      480
217 Ser Met Ser Trp Asp Asn Glu Val Ala Phe Asn Asn Gly Ser Gly Ser
218      485      490      495
221 Gly Asp Gly Ile Asp Lys Pro Val Val Pro Glu Gln Pro Asp Glu Pro
222      500      505      510
225 Gly Glu Ile Glu Pro Ile Pro Glu
226      515      520

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229 &lt;210&gt; SEQ ID NO: 3

230 &lt;211&gt; LENGTH: 990

231 &lt;212&gt; TYPE: DNA

232 &lt;213&gt; ORGANISM: Staphylococcus aureus

234 &lt;400&gt; SEQUENCE: 3

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235 gtagctgcag atgcaccggc agctggcaca gatattacga atcagttgac gaatgtgaca      60
237 gttgggtattg actctggtac gactgtgtat ccgcaccaag caggttatgt caaactgaat      120
239 tatgggttttt cagtgcctaa ttctgctgtt aaagggtgaca cattcaaaat aactgtacct      180
241 aaagaattaa acttaaatgg tgtaacttca actgctaaag tgccaccaat tatggctgga      240
243 gatcaagtat tggcaaatgg tgtaatcgat agtgatggta atgttattta tacatttaca      300
245 gactatgtaa atactaaaga tgatgtaaaa gcaactttga ccatgcccgc ttatattgac      360
247 cctgaaaatg ttaaaaagac aggtaatgtg acattggcta ctggcatagg tagtacaaca      420
249 gcaaacaaaa cagtattagt agattatgaa aaatatggta agttttataa cttatctatt      480
251 aaagggtacaa ttgaccaa atcgataaaaca aataatacgt atcgtcagac aatttatgtc      540
253 aatccaaagtg gagataacgt tattgcgccg gttttaacag gtaatttaaa accaaatagc      600
255 gatagtaatg cattaataga tcagcaaaat acaagtatta aagtatataa agtagataat      660
257 gcagctgatt tatctgaaag ttactttgtg aatccagaaa actttgagga tgtcactaat      720
259 agtgtgaata ttacattccc aaatccaaat caatataaag tagagtttaa tacgcctgat      780
261 gatcaaatta caacaccgta tatagtagtt gttaatggtc atattgatcc gaatagcaaa      840
263 ggtgatttag ctttacgttc aactttatat ggggtataact cgaatataat ttggcgctct      900

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265 atgtcatggg acaacgaagt agcatttaat aacggatcag gttctggtga cggtatcgat 960
267 aaaccagttg ttcctgaaca acctgatgag 990
270 <210> SEQ ID NO: 4
271 <211> LENGTH: 331
272 <212> TYPE: PRT
273 <213> ORGANISM: Staphylococcus aureus
275 <400> SEQUENCE: 4
277 Met Val Ala Ala Asp Ala Pro Ala Ala Gly Thr Asp Ile Thr Asn Gln
278 1 5 10 15
281 Leu Thr Asn Val Thr Val Gly Ile Asp Ser Gly Thr Thr Val Tyr Pro
282 20 25 30
285 His Gln Ala Gly Tyr Val Lys Leu Asn Tyr Gly Phe Ser Val Pro Asn
286 35 40 45
289 Ser Ala Val Lys Gly Asp Thr Phe Lys Ile Thr Val Pro Lys Glu Leu
290 50 55 60
293 Asn Leu Asn Gly Val Thr Ser Thr Ala Lys Val Pro Pro Ile Met Ala
294 65 70 75 80
297 Gly Asp Gln Val Leu Ala Asn Gly Val Ile Asp Ser Asp Gly Asn Val
298 85 90 95
301 Ile Tyr Thr Phe Thr Asp Tyr Val Asn Thr Lys Asp Asp Val Lys Ala
302 100 105 110
305 Thr Leu Thr Met Pro Ala Tyr Ile Asp Pro Glu Asn Val Lys Lys Thr
306 115 120 125
309 Gly Asn Val Thr Leu Ala Thr Gly Ile Gly Ser Thr Thr Ala Asn Lys
310 130 135 140
313 Thr Val Leu Val Asp Tyr Glu Lys Tyr Gly Lys Phe Tyr Asn Leu Ser
314 145 150 155 160
317 Ile Lys Gly Thr Ile Asp Gln Ile Asp Lys Thr Asn Asn Thr Tyr Arg
318 165 170 175
321 Gln Thr Ile Tyr Val Asn Pro Ser Gly Asp Asn Val Ile Ala Pro Val
322 180 185 190
325 Leu Thr Gly Asn Leu Lys Pro Asn Thr Asp Ser Asn Ala Leu Ile Asp
326 195 200 205
329 Gln Gln Asn Thr Ser Ile Lys Val Tyr Lys Val Asp Asn Ala Ala Asp
330 210 215 220
333 Leu Ser Glu Ser Tyr Phe Val Asn Pro Glu Asn Phe Glu Asp Val Thr
334 225 230 235 240
337 Asn Ser Val Asn Ile Thr Phe Pro Asn Pro Asn Gln Tyr Lys Val Glu
338 245 250 255
341 Phe Asn Thr Pro Asp Asp Gln Ile Thr Thr Pro Tyr Ile Val Val Val
342 260 265 270
345 Asn Gly His Ile Asp Pro Asn Ser Lys Gly Asp Leu Ala Leu Arg Ser
346 275 280 285
349 Thr Leu Tyr Gly Tyr Asn Ser Asn Ile Ile Trp Arg Ser Met Ser Trp
350 290 295 300
353 Asp Asn Glu Val Ala Phe Asn Asn Gly Ser Gly Ser Gly Asp Gly Ile
354 305 310 315 320
357 Asp Lys Pro Val Val Pro Glu Gln Pro Asp Glu
358 325 330

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361 <210> SEQ ID NO: 5
362 <211> LENGTH: 336
363 <212> TYPE: DNA
364 <213> ORGANISM: Staphylococcus aureus
366 <400> SEQUENCE: 5
367 aacattatga tgacacagtc gccatcatct ctggtgtgt ctgcaggaga aaaggtcact      60
369 atgagctgta agtccagtca aagtgtttta tacagttcaa atcagaagaa ctacttggcc      120
371 tggtagcagc agaaaccagg gcagtctcct aaactactga tctactgggc atccactagg      180
373 gaatctggtg tcctgatcg cttcacaggc agtggatctg ggacagattt tactcttacc      240
375 atcaacagtg tacaagctga agacctggca gtttattact gtcataata cctctcctcg      300
377 cacacgttcg gaggggggac caagctggaa ataaaa      336
380 <210> SEQ ID NO: 6
381 <211> LENGTH: 112
382 <212> TYPE: PRT
383 <213> ORGANISM: Staphylococcus aureus
385 <400> SEQUENCE: 6
387 Asn Ile Met Met Thr Gln Ser Pro Ser Ser Leu Ala Val Ser Ala Gly
388 1      5      10      15
391 Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser
392      20      25      30
395 Ser Asn Gln Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
396      35      40      45
399 Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
400      50      55      60
403 Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
404 65      70      75      80
407 Ile Asn Ser Val Gln Ala Glu Asp Leu Ala Val Tyr Tyr Cys His Gln
408      85      90      95
411 Tyr Leu Ser Ser His Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
412      100      105      110
415 <210> SEQ ID NO: 7
416 <211> LENGTH: 354
417 <212> TYPE: DNA
418 <213> ORGANISM: Staphylococcus aureus
420 <400> SEQUENCE: 7
421 caggtgcatc tgaaggagtc aggacctggc ctggtggcac cctcacagag cctgtccatc      60
423 acatgcactg tctctggatt ctattatcc agatataata tacactgggt tcgccagcct      120
425 ccaggaaagg gtctggagtg gctgggaatg atatggggtg gtgaaaacac agactataat      180
427 tcagctctca aatccagact gagcatcagc aaggacaact ccaagagcca agttttctta      240
429 aaaatgaaca gtctgcaaac tgatgacaca gccatgtact actgtgccag cgcctactat      300
431 ggtaactcct ggtttgctta ctggggccag gggactctgg tcaactgtctc tgca      354
434 <210> SEQ ID NO: 8
435 <211> LENGTH: 118
436 <212> TYPE: PRT
437 <213> ORGANISM: Staphylococcus aureus
439 <400> SEQUENCE: 8
441 Gln Val His Leu Lys Glu Ser Gly Pro Gly Leu Val Ala Pro Ser Gln
442 1      5      10      15
445 Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Ser Arg Tyr

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Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 12,13

VERIFICATION SUMMARY

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Input Set : A:\Sequence\_10-056,152.txt

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L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date